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OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/071,866

DATE: 02/26/2002

TIME: 13:43:44

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02262002\J071866.raw

ENTERED

3 <110> APPLICANT: Hua, Shao-bing
 4 Pauling, Michelle H.
 5 Zhu, Li
 7 <120> TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY
 AGAINST PEPTIDE
 8 FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
 10 <130> FILE REFERENCE: 25636-717
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/071,866
 C--> 12 <141> CURRENT FILING DATE: 2002-02-08
 12 <160> NUMBER OF SEQ ID NOS: 54
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 352
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
 23 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
 24 1 5 10 15
 27 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
 28 20 25 30
 31 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
 32 35 40 45
 35 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
 36 50 55 60
 39 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
 40 65 70 75 80
 43 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
 44 85 90 95
 47 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
 48 100 105 110
 51 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
 52 115 120 125
 55 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
 56 130 135 140
 59 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
 60 145 150 155 160
 63 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
 64 165 170 175
 67 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
 68 180 185 190
 71 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
 72 195 200 205
 75 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
 76 210 215 220

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79 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
80 225                230                235                240
83 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
84                245                250                255
87 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
88                260                265                270
91 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
92                275                280                285
95 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
96                290                295                300
99 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
100 305                310                315                320
103 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
104                325                330                335
107 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
108                340                345                350
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 17
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 2
118 Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp
119 1                5                10                15
122 Gln
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 29
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 3
133 Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln
134 1                5                10                15
137 Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys
138                20                25
141 <210> SEQ ID NO: 4
142 <211> LENGTH: 20
143 <212> TYPE: PRT
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: G4S Linker
149 <400> SEQUENCE: 4
151 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
152 1                5                10                15
155 Gly Gly Gly Ser
156                20
159 <210> SEQ ID NO: 5
160 <211> LENGTH: 60
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:

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165 <223> OTHER INFORMATION: DNA of G4S Linker
167 <400> SEQUENCE: 5
168 ggcgggtggtg gatcaggcgg cggaggatct ggcggaggtg gcagcgggtg tggaggcagt      60
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 60
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: 5' Homologous Sequence
179 <400> SEQUENCE: 6
180 accccaccaa acccaaaaaa agagatctgt atggcttacc catacgaatgt tccagattac      60
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 57
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: 3' Homologous Sequence
191 <400> SEQUENCE: 7
192 gagatggtgc acgatgcaca gttgaagtga acttgcgggg tttttcagta tctacga      57
195 <210> SEQ ID NO: 8
196 <211> LENGTH: 36
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 8
202 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
203 1          5          10          15
206 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
207          20          25          30
210 Leu Pro Pro Leu
211          35
214 <210> SEQ ID NO: 9
215 <211> LENGTH: 32
216 <212> TYPE: PRT
217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 9
221 Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe
222 1          5          10          15
225 Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile
226          20          25          30
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 30
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Primer
237 <400> SEQUENCE: 10
238 ggagaattcg attatcaagt gtcaagtcca      30
241 <210> SEQ ID NO: 11
242 <211> LENGTH: 31

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243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Primer
249 <400> SEQUENCE: 11
250 cgcggatcct tagagcggag gcaggaggcg g 31
253 <210> SEQ ID NO: 12
254 <211> LENGTH: 29
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Primer
261 <400> SEQUENCE: 12
262 ggagaattca ccagatctca aaaagaagg 29
265 <210> SEQ ID NO: 13
266 <211> LENGTH: 33
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Primer
273 <400> SEQUENCE: 13
274 cgcggatcct tatatcttta atgtctggaa att 33
277 <210> SEQ ID NO: 14
278 <211> LENGTH: 21
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Primer
285 <400> SEQUENCE: 14
286 caggaattct ttggcctgaa t 21
289 <210> SEQ ID NO: 15
290 <211> LENGTH: 31
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Primer
297 <400> SEQUENCE: 15
298 cgcggatcct cagcagtgcg tcatcccaag a 31
301 <210> SEQ ID NO: 16
302 <211> LENGTH: 759
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Clone 15.186.35
309 <400> SEQUENCE: 16
310 caggttacct tgaaggagtc tggtcctacg ttggtgaaac ccacacagac cctcacgctg 60
312 acctgcacct tgtctgggtt ctactcagc actagtggag tgagtgtggg ctggatccgt 120
314 cagccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc 180
316 tacagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccaggtg 240

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318 gtccttgcaa tgaagcaacat ggaccctgcy gacacagcca catattcctg tgcactcgat 300
320 atgccccccc atgatagtggt cccgcaatct tttgatgctt ctgatgtctg gggcccaggg 360
322 acaatgggtca ccgtctcttc aggcggtggt ggatcaggcg gcggaggatc tggcggaggt 420
324 ggcagcggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc 480
326 ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc 540
328 tggatatcaac agaagccagg ccggtccccct gtgctggtca tttatggaga taacaagcgg 600
330 ccctcaggga tccctgagcg attctctggc tccaactctg ggaacacagc cactctgacc 660
332 atcagcgagg cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc 720
334 actgctgtct tcggaactgg gaccaagctc accgtccta 759
337 <210> SEQ ID NO: 17
338 <211> LENGTH: 253
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Clone 15.186.35
345 <400> SEQUENCE: 17
347 Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
348 1 5 10 15
351 Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
352 20 25 30
355 Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
356 35 40 45
359 Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
360 50 55 60
363 Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
364 65 70 75 80
367 Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
368 85 90 95
371 Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
372 100 105 110
375 Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly
376 115 120 125
379 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
380 130 135 140
383 Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser
384 145 150 155 160
387 Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp
388 165 170 175
391 Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu
392 180 185 190
395 Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
396 195 200 205
399 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
400 210 215 220
403 Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser
404 225 230 235 240
407 Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
408 245 250
411 <210> SEQ ID NO: 18

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\PTO.VSK.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32

L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33